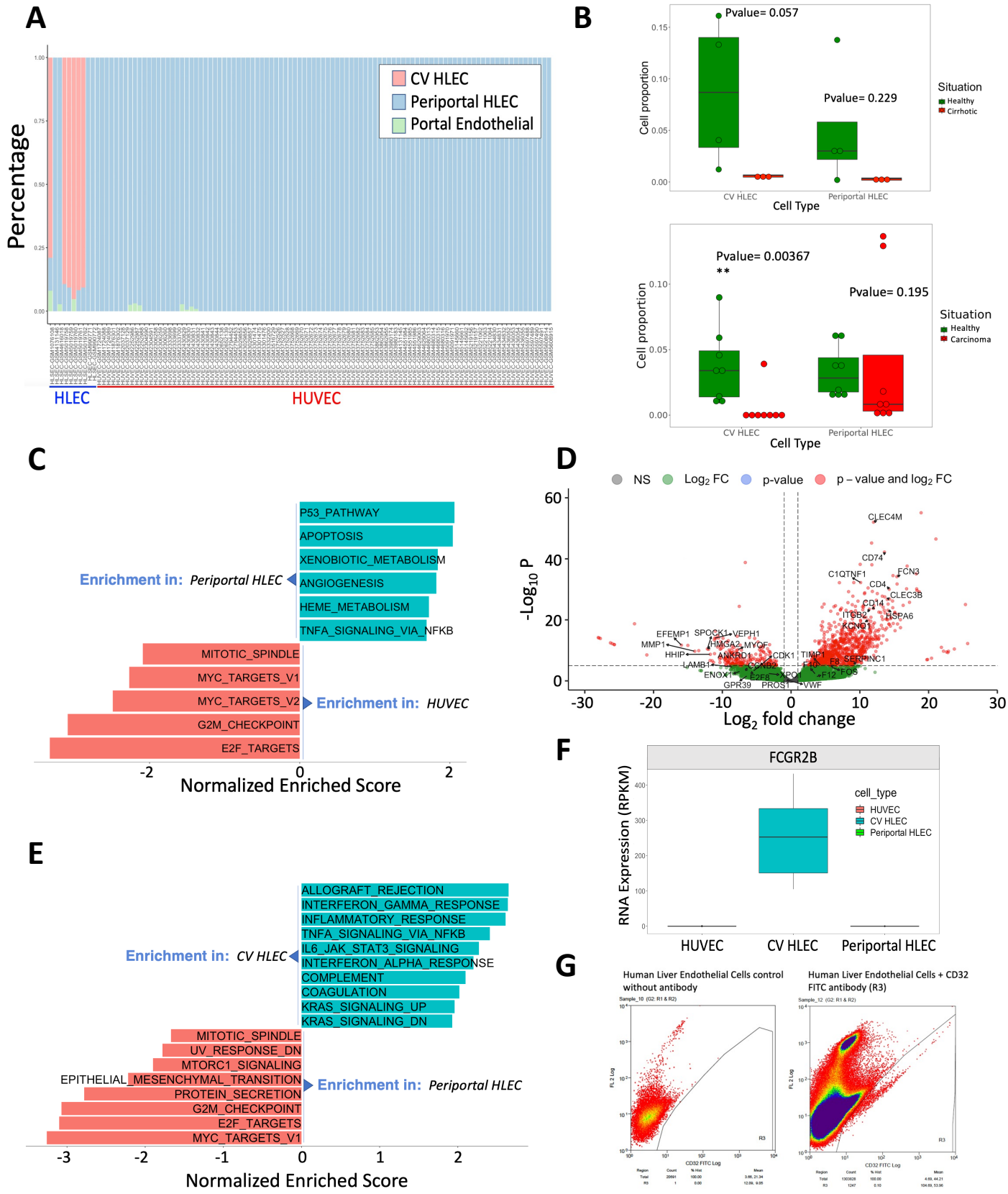
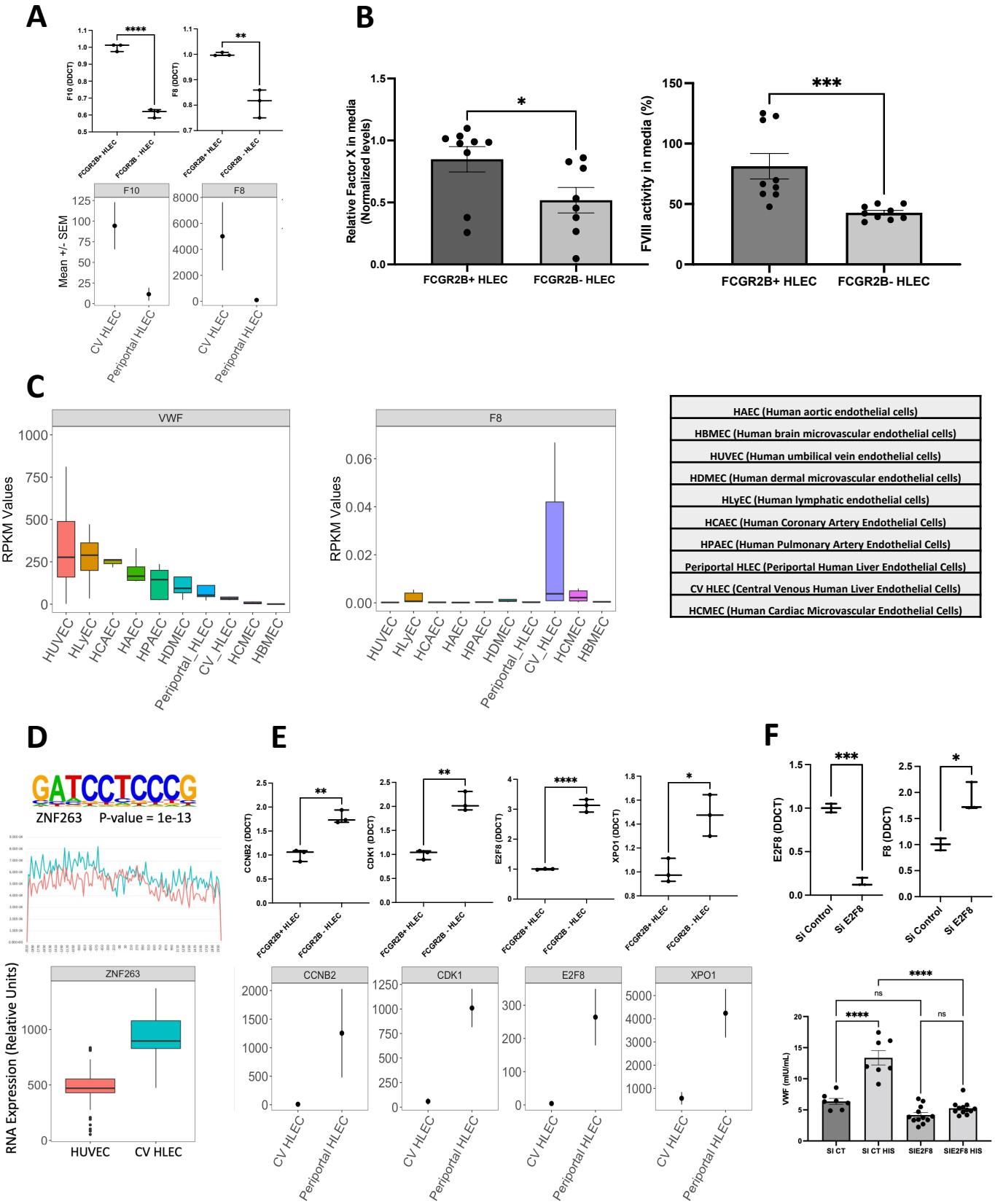
Supplemental figure 1



(**A**) Representation using Cibersortx of the percentage of correspondence between the HLEC samples identified as distinct from the vascular endothelium by PCA and Central venous (CV) HLEC, periportal HLEC and portal endothelial cells, (**B**) Analysis from single cell RNA-seq data including healthy participants and participants with cirrhosis or hepatocellular carcinoma, showing cell proportion of CV HLEC and Periportal HLEC in both situations, (**C**) Gene set enrichment analysis revealing the HALLMARK enriched pathways in periportal HLEC and HUVEC at FDR<0.05, (**D**) Volcano Plot presenting the transcriptional differences between CV HLEC and Periportal HLEC (CV HLEC upregulated genes on the right), (**E**) Gene set enrichment analysis revealing the HALLMARK enriched pathways in CV HLEC and Periportal HLEC at FDR<0.05, (**F**) Boxplot showing the differences in the expression of FCGR2B in HUVEC, CV HLEC and periportal HLEC which appears to be uniquely present in CV HLEC, (**G**) Process of purification of CV HLEC by sorting commercially obtained HLEC based on surface FCGR2B expression.

Supplemental figure 2



(**A**) RT-qPCR based (upper panel) and bulk RNA-seq (lower panel) expression of coagulation genes (F10, F8) in FCGR2B+ HLEC and FCGR2B- HLEC (results presented in Mean +/- SEM), (**B**) ELISA of 24 hour supernatants of FCGR2B+ HLEC and FCGR2B- HLEC for FX and activity assay for FVIII in the supernatants, (**C**) Box plots comparing VWF and F8 expression in RPKM in different types of endothelial cells, (**D**) Prioritized de-novo motifs and corresponding enrichment of known ZNF263 motifs in CV HLEC and HUVEC (upper panel), box plot with the expression of ZNF263 in CV HLEC and HUVEC in bulk RNA-seq (lower panel), (**E**) RT-qPCR based (upper panel) and bulk RNA-seq (lower panel) expression of genes (CCNB2, CDK1, E2F8, XPO1) in FCGR2B+ HLEC and FCGR2B- HLEC (results presented in Mean +/- SEM), (**F**) HUVEC were transfected with oligonucleotides directed against E2F8 or a control sequence, mRNA for E2F8 and F8 was measured by RT-qPCR and ELISA was used for measuring VWF release with or without histamine (10uM) stimulation in HUVEC.